AMENDMENTS TO THE SPECIFICATION

Please replace the last paragraph on page 9 of the specification (which wraps around to the top of page 10) with the following replacement paragraph:

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package ~~(available at http://www.gcg.com)~~, using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al., Nucleic Acids Res. 12(1)*:387 (1984)) ~~(available at http://www.gcg.com)~~, using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

Please replace the "DESCRIPTION OF THE FIGURE SHEETS" section on page 4 of the specification with the following replacement section:

DESCRIPTION OF THE FIGURE SHEETS

FIGURES 1A-1B ~~1~~ provides the nucleotide sequence of a cDNA molecule or transcript sequence that encodes the secreted protein of the present invention. (SEQ ID NO:1) In addition, structure and functional information is provided, such as ATG start, stop and tissue distribution, where available, that allows one to readily determine specific uses of inventions based on this molecular sequence. Experimental data as provided in Figure 1 indicates expression in head/neck, nervous tumor, colon, breast, and placenta tissue.

FIGURES 2A-2F ~~2~~ provides the predicted amino acid sequence of the secreted protein of the present invention. (SEQ ID NO:2) In addition structure and functional information such as protein family, function, and modification sites is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence.

FIGURES A-3FF ~~3~~ provides genomic sequences that span the gene encoding the secreted protein of the present invention. (SEQ ID NO:3) In addition structure and functional information, such as intron/exon structure, promoter location, etc., is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence. As illustrated in Figure 3, SNPs were identified at 24 different nucleotide positions in the nephronectin gene of the present invention.

Please replace the third paragraph (at lines 11-18) on page 3 of the specification with the following paragraph:

Previous studies in the mouse have indicated that nephronectin is a ligand that binds and modulates integrin alpha8beta1 function in the embryonic kidney (Brandenberger ~~Schmidt~~ *et al., J Cell Biol* 2001 Jul 23;154(2):447-58). Mice lacking integrin alpha8beta1 display deficient epithelial-mesenchymal interactions, which are

necessary for proper kidney organogenesis. Furthermore, because nephronectin is widely expressed outside the kidney, it has been suggested that nephronectin plays wider roles in development (Brandenberger ~~Schmidt~~ *et al., J Cell Biol* 2001 Jul 23;154(2):447-58). Therefore, novel human nephronectin splice forms are particularly useful as therapeutic targets for treating developmental disorders.